

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Sep 13 18:13:05 EDT 2007

=====

Application No: 10578234 Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-04 13:36:46.672

Finished: 2007-09-04 13:36:47.304

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 632 ms

Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 24

Actual SeqID Count: 24

# SEQUENCE LISTING

<110> CuraGen Corporation et al.  
 Alsobrook II, John P.  
 Eichen, Joseph  
 Lepley, Denise M.  
 Miller, Charles E.  
 Mezes, Peter

<120> COMPOSITIONS AND METHODS OF USE FOR A FIBROBLAST GROWTH FACTOR

<130> 15966-557 SNP NATL (Cura-57 SNP NATL)

<140> 10578234

<141> 2007-09-04

<150> 10/702,126

<151> 2003-11-04

<160> 24

<170> CuraSeqList version 0.1

<210> 1

<211> 633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(633)

<400> 1

atg gct ccc tta gcc gaa gtc ggg ggc ttt ctg ggc ggc ctg gag ggc	48
Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly	
1 5 10 15	

ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc ggg gag	96
Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu	
20 25 30	

cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gcg gag ccg agc gcg	144
Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala	
35 40 45	

cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg	192
Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu	
50 55 60	

cgc cgc ccg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg	240
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
65 70 75 80	

ccc gac ggc agc gtg cag ggc acc ccg cag gac cac agc ctc ttc ggt	288
Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
85 90 95	

atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt	336
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly	
100 105 110	

gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat	384
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
115 120 125	

gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa	432
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
130 135 140	

gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac	480
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp	
145 150 155 160	

act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga	528
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg	
165 170 175	

gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct	576
Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro	
180 185 190	

aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag aac cta ctg	624
Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu	
195 200 205	

atg tac act	633
Met Tyr Thr	
210	

<210> 2  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 2	
Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly	
1 5 10 15	
Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu	
20 25 30	
Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala	
35 40 45	
Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu	
50 55 60	
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
65 70 75 80	
Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
85 90 95	

Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly  
100 105 110

Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr  
115 120 125

Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu  
130 135 140

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp  
145 150 155 160

Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg  
165 170 175

Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro  
180 185 190

Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu  
195 200 205

Met Tyr Thr  
210

<210> 3  
<211> 633  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(633)

<400> 3  
atg gct ccc tta gcc gaa gtc ggg ggc ttt ctg ggc ggc ctg gag ggc 48  
Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly  
1 5 10 15  
ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc ggg gag 96  
Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu  
20 25 30  
cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gcg gag ccg agc gcg 144  
Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala  
35 40 45  
cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg 192  
Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu  
50 55 60  
cgc cgc ccg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg 240  
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu  
65 70 75 80  
ccc gac ggc agc gtg cag ggc acc ccg cag gac cac agc ctc ttc ggt 288  
Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly  
85 90 95

atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt	336
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly	
100 105 110	

gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat	384
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
115 120 125	

gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa	432
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
130 135 140	

gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac	480
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp	
145 150 155 160	

act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga	528
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg	
165 170 175	

gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct	576
Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro	
180 185 190	

aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac cta ctg	624
Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu	
195 200 205	

atg tac act	633
Met Tyr Thr	
210	

<210> 4  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 4	
Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly	
1 5 10 15	
Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu	
20 25 30	
Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala	
35 40 45	
Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu	
50 55 60	
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
65 70 75 80	
Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
85 90 95	

Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly  
100 105 110

Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr  
115 120 125

Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu  
130 135 140

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp  
145 150 155 160

Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg  
165 170 175

Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro  
180 185 190

Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu  
195 200 205

Met Tyr Thr  
210

<210> 5  
<211> 477  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(474)

<400> 5  
atg gct cag ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg 48  
Met Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu  
1 5 10 15

tac tgc cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt 96  
Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val  
20 25 30

cag ggt acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc 144  
Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile  
35 40 45

tct gtt gct gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg 192  
Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu  
50 55 60

tac ctg ggt atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg 240  
Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu  
65 70 75 80

acc tct gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac 288  
Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn  
85 90 95

acc tac tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac 336  
 Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr  
 100 105 110

ttc gtt gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct 384  
 Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser  
 115 120 125

aaa cgt cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg 432  
 Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro  
 130 135 140

gag cgt gtt cca gaa ctg tat aaa aac ctg ctg atg tac acc taa 477  
 Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr  
 145 150 155

<210> 6  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu  
 1 5 10 15

Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val  
 20 25 30

Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile  
 35 40 45

Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu  
 50 55 60

Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu  
 65 70 75 80

Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn  
 85 90 95

Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr  
 100 105 110

Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser  
 115 120 125

Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro  
 130 135 140

Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr  
 145 150 155

<210> 7  
 <211> 540  
 <212> DNA  
 <213> Homo sapiens



<220>

<221> CDS

<222> (1)..(537)

<400> 7

atg gct ccc tta gcc gaa gtc ggg ggc ttt ctg ggc ggc ctg gag ggc	48
Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly	
1 5 10 15	

ttg ggc cag ccg ggg gca gcg cag ctg gcg cac ctg cac ggc atc ctg	96
Leu Gly Gln Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu	
20 25 30	

cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg	144
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
35 40 45	

ccc gac ggc agc gcg cag ggc acc cgg cag gac cac agc ctc ttc ggt	192
Pro Asp Gly Ser Ala Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
50 55 60	

atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt	240
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly	
65 70 75 80	

gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat	288
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
85 90 95	

gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa	336
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
100 105 110	

gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac	384
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp	
115 120 125	

act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga	432
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg	
130 135 140	

gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct	480
Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro	
145 150 155 160	

aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag aac cta ctg	528
Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu	
165 170 175	

atg tac act tag	540
Met Tyr Thr	

<210> 8

<211> 179

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly  
1 5 10 15

Leu Gly Gln Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu  
20 25 30

Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu  
35 40 45

Pro Asp Gly Ser Ala Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly  
50 55 60

Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly  
65 70 75 80

Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr  
85 90 95

Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu  
100 105 110

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp  
115 120 125

Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg  
130 135 140

Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro  
145 150 155 160

Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu  
165 170 175

Met Tyr Thr

<210> 9

<211> 636

<212> DNA

<213> Homo sapiens

<400> 9

atggctccgc tggctgaagt tgggtggtttc ctgggcgggc tggagggtct gggtcagcag 60  
gttggttctc acttcctgct gccgccggct ggtgaacgtc cgccactgct ggggtgaacgt 120  
cgctccgcag ctgaacgtc cgctcggttg ggcccgggtg ctgctcagct ggctcacctg 180  
catggtatcc tgcgtcgccg tcagctgtac tgccgtactg gtttccacct gcagatcctg 240  
ccggatgggt ctgttcaggg taccgcgcag gaccactctc tggtcgggtat cctggaattc 300  
atctctgttg ctgttggtct ggtttctatc